Graphic Maps

Standard Graphic Maps:

With a working map on screen, click Settings button to set style and color options for the standard graphic maps. These settings are remembered and will provide consistent, standard high-resolution graphic maps until changed.

For special features, click to select feature and click Tools, Customize Feature Style to set custom feature style or color for this one feature.

Click Content tab on Settings dialog box to select a map style that adds descriptive text to the map page, a good choice for your notebook.

Enhanced Views:

With a working map on screen, click Enhanced View button and select New View to create a special graphic map that you can customize to use for a presentation or publication. Drag lower right corner to increase size of map window. Delete non-essential enzyme sites or features in this view without removing them from your molecule file.

Basic Settings -- click Settings, Map Basics to set basic options for the molecule map (format, size, basepair intervals, line widths).

Click Settings, Feature Basics to set feature font styles and colors.

Click Settings, Enzyme/primer/label Site Basics to set fonts and colors for map sites, or to show basepair numbers or italicize the first three letters of enzyme names.

Special Feature settings -- click on a feature to select. Then use toolbar buttons to change position, style, pattern, color for this one feature. Drag feature name to reposition, if needed.

Text -- click on text to select and then use toolbar controls to change font face, point size, color. All enzyme names use the same font and color; all feature names use the same font but can be in different colors.

Save Enhanced View -- click Save or Send button to save this enhanced view to the molecule file (maximum 6 per file). Remember to save the modified molecule file to disk before exiting the program.

Print, Copy, Export Maps:

Click toolbar Print button to send the standard or enhanced view graphic map to your printer.

Click toolbar Send View to Clipboard button to copy the map for use in other applications. Use Edit, Paste Special to paste map into a word processing document.

Click toolbar Send View to File button to prepare a Windows Metafile (emf or wmf) for use in other Windows applications.

Click button Save for Web on map window toolbar to prepare a raster graphic file in png format for web page or on-screen presentations.

For enhanced views, click Save or Send button in enhanced view window to copy to the clipboard or export to file in vector (wmf, emf) or raster (GIF, TIF, PNG) formats at high or low resolution.

Quick Reference
Clone Manager 10
for Windows

Getting Started

To install an individual or workgroup copy, insert the program CD in drive and allow disk to autorun. Follow the instructions on your screen.

Double-click the Clone Manager icon to start the program.

Getting Help -- click File, Help or use toolbar Help button to view complete application help. In Help, click Show to open Search pane to find topics with specific keywords.

Click File, Preferences to set author name, default save format, or features to import when loading files in GenBank or EMBL formats.

Working with Molecules

Open Files -- Load Molecules:

Click File, Open or use Open toolbar button. Use Shift or Control keys in conjunction with mouse to open more than one file at the same time.

Information on the clipboard can be read as if it were a disk file using File, Other Tools > Import from Clipboard. Or use the Paste Sequence option found in the New Molecule dialog box.

Click File, Other Tools > Retrieve from Entrez eUtils to find sequence files at the NCBI. With the search results on the screen, click to select a file. Click button Show GenBank File to view or Get Molecule to import molecule for immediate use.

Click Find in Files toolbar button to locate molecule files containing specified feature or text.

Creating new molecules:

Click File, New and then follow the wizard instructions to create a new molecule. Save new molecule to disk when complete.

Selecting molecules:

Active molecule is in active window (dark title bar). Click on a different window to change the active molecule or select from Molecule List.

Click Molecule List toolbar button to access list of loaded molecules. Click More Info/Less Info to display or hide additional information that can help you select the needed molecule. Asterisk symbol marks unsaved new or modified molecules.

Molecule Viewer Window

Click tabs at the bottom of the window to see molecule Map, Restriction Map data, Sequence, Features or molecule Information. Click Zoom button in tab region (left) to temporarily view just a part of the molecule.

Map Tab -- Working Map display

Enzyme sites, primer sites and label sites can appear on the working map along with features (genes, regions, markers). Click Change Sites button to select.

Point to a site or feature on the map to see basepair position information and suppressed enzyme sites in crowded areas (++ notation), if present. Click on site or feature and then use toolbar buttons to view site properties, go to sequence at site, or take other action.

Click Find button to Find Enzyme Sites (AutoScan) to scan for enzyme sites, Find ORFs to locate open reading frames, enter as genes.

Click Enhanced View button then select New View to start an enhanced map of this molecule.

Click Settings button, Screen Basics to set working map display options.

RMap Tab -- Restriction Map data

Click column headers to sort by enzyme name or number of sites. Click Select View button to select display style, including No Cutters (enzymes that do not cut this molecule). Select a different enzyme list and regenerate restriction map data.

Click Settings button to set display styles and remember settings. Click Filter button to set filter options to limit data displayed. Click again to remove filter. Click on an enzyme and then use toolbar buttons to view enzyme properties, suppliers, isoschizomers or compatible ends information. Click Tools to add enzyme sites to the map, or cut with this enzyme.

Sequence Tab -- Sequence data

View, edit or format molecule sequence. Click Settings button to set sequence display styles and colors and memorize settings. Click My Style button to format sequence using your memorized settings.

Edit sequence -- click the Edit Sequence button to change the sequence by adding or removing bases. You can also use cut, copy and paste operations on sequence data. Sequence is stored in the program single-stranded and all operations work on the upper strand of sequence.

Features Tab -- Features table

Click Features tab to view features table and add or edit information about molecule features. Click Feature properties button to see codon usage, amino acid composition, molecular weight and pI for gene translation products. Click GB Location/Qualifiers button see join segment data.

Click Customize button to set custom feature styles for map or sequence. Click Settings button to display or hide information-only features. Click Filter to limit by feature type or location.

Info Tab -- Molecule information

Click Info tab to view or edit molecule name, description, translation table setting, notes, starting bp number, or view molecule composition.

Enzyme Operations

Find Enzyme sites:

Click Clone, Find Enzyme Sites to find sites for specific enzymes or all enzymes on a list that meet a specific requirement (like single cutters) or all enzymes on a user list.

View or build enzyme lists:

To view, click Enzyme Lists toolbar button. To edit a user list, click the Edit User List button, unlock the list and then add or delete enzymes. To build a new user list, click the Build User List button.

REBASE updates:

Click Enzyme Lists and then click the REBASE Update button to update your master enzyme file using the latest REBASE data file (updated monthly). Each time you update, the Commercial (Main), All Enzymes, and Scanner enzyme lists will be regenerated. User enzyme lists and any special enzymes you entered will not be affected.

Instant enzyme information:

Click toolbar buttons on the Map, RMap or Enzyme List displays to view enzyme information (Properties, Suppliers, Isoschizomers or Compatible Ends). Enzyme information is updated when you do a REBASE update.

Cloning Operations

Cut molecules:

Click Clone, Cut or use button on ligate display to cut a molecule with specific enzymes, cut at a single map site, or cut at specified bp positions.

Modify molecule ends:

Click Clone, Modify Ends or use button on ligate display. Use Klenow Fill-In, 5'->3' or 3'->5' exonuclease, Partial Fill-In, or custom modification.

Ligate molecules:

Click Clone, Ligate to join together two or more pieces of DNA or join the ends of the same molecule (self-ligate). Use toolbar buttons to add or move molecules so that fragments are in order of ligation. Small icons appear between fragment boxes to indicate if ligation is possible.

Click on a fragment to make it active (appears in upper window), then use buttons to cut, modify ends, or invert molecule as needed for ligation.

Use the Cloning Wizards:

Click Clone, Plan Cloning to define what you want to clone and which vector to use. Set your enzyme and cloning preferences (or use default settings). Review the possible solutions listed, construct the recombinant of choice, or redefine the procedure.

Click Clone then select Gateway Cloning, Topoisomerase Cloning, or one of the assembly cloning wizards to simulate cloning using these techniques. Use the Ligation-Independent Cloning wizard to join fragments previously prepared with correct overlaps. Use the Gibson Cloning or In-Fusion cloning wizards to use PCR to create amplified fragments with overlaps.

The wizards will help you select the appropriate components, show you the proposed result, and create the final recombinant molecule.